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; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9166
; LENGTH: 423
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9166

Alignment Scores:
Pred. No.: 0.0709 Length: 423
Score: 113.50 Matches: 36
Percent Similarity: 36.65% Conservative: 23
Best Local Similarity: 22.36% Mismatches: 57
Query Match: 9.07% Indels: 46
Gaps: 3
DB: 1

US-09-252-991A-26292 (1-245) x US-09-252-991A-9166 (1-423)

QY 44 AlaArgGluValMetLeuGluLeuValAlaThrGlyGlnLeuThrAspProGluSerAla 63
DB 384 GCCCGCAAGCCTCGCGCGGAGATGATC-----GAGAAACC 349
QY 64 ArgGlyLysLeuGlnThrAlaAlaHisLeuPheArgSerLysGlyTyrGluArgThr 83
DB 348 CGCGCCAGCTGATGAGACGCCGCCGAGCGCTTCCGCCACACGCGCTACGCCGCC 289
QY 84 ThrValArgAspLeuAlaSerAlaValGlyIleGlnSerGlySerIlePheHisPhe 103
DB 288 TCGATGACAGCTGACCGCGCGCGCTCACCGCGCGCTGATACACACTTC 229
QY 104 LysSerLysAspGluIleLeuArgSerValMetGluGlnThrIleLeuTyrAsnThrAla 123
DB 228 GCCGCAAGAAAGCGCTCTCGCGCGGTGTGACGACGACGACGACGATGATCTT 169
QY 124 LeuMetArgAlaAlaLeuAlaAspAlaGluAspLeuArgValArgValLeuGlyLeuIle 143
DB 168 CGCGTGGCGGCTATCTGCTGCTCGCGCGGAGACCTC----- 133
QY 144 ArgCysGluLeuGlnSerIleMetGlyGlyThrGlyGluAlaMetAlaValLeuValTyr 163
DB 133 ----- 133
QY 164 GluTrpArgSerLeuSerAlaGluGlyGlnAlaTyrIleLeuGlyLeuArgAspIleTyr 183
DB 132 ---TGGAGCGGCTTCCTGCTCAACACGCGGCTACCTG----- 97
QY 184 GluIleMetTrpLeuAspValLeuGlyGluAlaArgLeuAlaGlyTyrCysGlnGlyAsp 203
DB 96 ---GAATGGCCCTGGAAGCGGA-AAATCCAGCGCATGCTCTGCGCATGCCGCGCAT 41
QY 204 Pro 204
DB 40 CCT 38

RESULT 11
US-09-252-991A-1993
; Sequence 1993, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7804
; LENGTH: 702
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7804

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; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1993
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1993

Alignment Scores:
Pred. No.: 0.146 Length: 654
Score: 113.50 Matches: 35
Percent Similarity: 50.98% Conservative: 17
Best Local Similarity: 34.31% Mismatches: 27
Query Match: 9.07% Indels: 23
Gaps: 4
DB: 1

US-09-252-991A-26292 (1-245) x US-09-252-991A-1993 (1-654)

QY 66 LysLeuLeuGlnThrAlaAlaHisLeuPheArgSerLysGlyTyrGluArgThrThrVal 85
DB 64 GAGATTCGATATCCGCTCAAGCTGTTCTCGAAGCGGGGAGACAGCGCTAACGGTC 123
QY 86 ArgAspLeuAlaSerAlaValGlyIleGlnSerGlySerIlePheHisPheLysSer 105
DB 124 GAGATGATCGCGGATCGCGCTCGCATCGCAAGACAGCATCTTCAAGCACTCAAGTCC 183
QY 106 LysAspGluIleLeuArgSerValMetGluGlnThrIleLeuTyrAsnThrAlaLeuMet 125
DB 184 AAGCGGAGATCTACTCGCGCTGATGCTGAC-----TAGACCGGATCTC--- 231
QY 126 ArgAlaAlaLeuAlaAspAlaGluAspLeu---ArgGluArgValLeuGlyLeuIleArg 144
DB 232 ---GCCGCTGTTCCATCTTCGAAAGCATGACCGCGACAG----- 270
QY 145 CysGluLeuGlnSerIleMetGlyGlyThrGlyGluAlaMetAlaValLeuValTyrGlu 164
DB 271 -----GAAGCCCTGTCTGCGCGCTACTTCCAG 297
QY 165 TrpArg 166
DB 298 TTCCGC 303

RESULT 12
US-09-252-991A-7804
; Sequence 7804, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7804
; LENGTH: 702
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7804

Alignment Scores:
Pred. No.: 0.193 Length: 702
Score: 112.50 Matches: 52
Percent Similarity: 41.62% Conservative: 30
Best Local Similarity: 26.40% Mismatches: 84

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;; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;; FILE REFERENCE: 107196.136
;; CURRENT APPLICATION NUMBER: US/09/252,991A
;; PRIOR FILING DATE: 1999-02-18
;; PRIOR APPLICATION NUMBER: US 60/074,788
;; PRIOR FILING DATE: 1998-02-18
;; PRIOR APPLICATION NUMBER: US 60/094,190
;; PRIOR FILING DATE: 1998-07-27
;; NUMBER OF SEQ ID NOS: 33142
;; SEQ ID NO 8914
;; LENGTH: 618
;; TYPE: DNA
;; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8914

Alignment Scores:
Pred. No.: 0.0953 Length: 618
Score: 115.50 Matches: 48
Percent Similarity: 42.25% Conservative: 31
Best Local Similarity: 25.67% Mismatches: 67
Query Match: 9.23% Indels: 41
DB: 1 Gaps: 8

US-09-252-991A-26292 (1-245) x US-09-252-991A-8914 (1-618)

OY 44 AAlaAGluValMetLeuGluLeuValAlaThrGlyInLeuThrAspProGluSerAla 63
DB 31 GCGCCCAAGCCCTCGCGCCGAGATGATC-----GAGGAACC 66
OY 64 ArgGlyLysLeuLeuGlnThrAlaAlaHisLeuPheArgSerLysGlyTrpGluArgThr 83
DB 67 CGCGCCAGCTGATGATGACGCGCGCGAGCTTCGCGCACACGCGTACGCGCGCGCC 126
OY 84 ThrValArgAspLeuAlaSerAlaValGlyIleGlnSerGlySerIlePheHisPhe 103
DB 127 TCGATGGAGCAACTGACCGCGCGCGCGCTCACCCGCGCGCGCTGATACCACTTC 186
OY 104 LysSerLysAspGluIleLeuArgSerValMetGluGluThrIleLeuTrpAsnThrAla 123
DB 167 GCGGCACMAAAGCGCTGTGCGCGCGGTGTCACAGATGACAGACAGATGATCTT 246
OY 124 LeuMetArgAlaAlaLeuAlaAspAlaGluAspLeu----- 135
DB 247 CGCCTCGCGCCATCTGTGCTGCGCGAGCATCTGTGAGCGGCTCCGCTCTACAC 306
OY 136 ArgGluArgValLeuGlyLeuLeuArgGlyGluLeuGlnSerIleMetClyLysThrGly 155
DB 307 CGGGCTACTCTGGAATGCGCTGTGAGCGGAATCCACGCGATCGTC-----CTGCGC 360
OY 156 GluAlaMetAlaValLeu-----ValTrpGluTrpArgSerLeuSer 169
DB 361 GATGCGCGCGCATCTCTGCGCGAGCCGACGACGAGCGACGACGACGCTGCTTAC 420
OY 170 Ala---GluGlyGlnAlaTrpIleLeuGlyLeuArgAspIleTrpGluInMetTrpLeu 188
DB 421 TCGATGACCGCGCAA-----CTGCGCGAATGATGACGAGC----- 456
OY 189 AspValLeuGluAlaAlaArgLeuAlaGlyTrpGlyGlnGlyAspProPheLeuArg 208
DB 457 -----GGGCGCGCTCGC-----CGACCGCGCGCGAGCGCTGCGC 492
OY 209 ArgPheLeuThrGlyAlaLeu 215
DB 493 TGGCTGCTCAACGGCGCGCTG 513

RESULT 9
US-09-252-991A-10401
; Sequence 10401, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

;; FILE REFERENCE: 107196.136
;; CURRENT APPLICATION NUMBER: US/09/252,991A
;; PRIOR FILING DATE: 1999-02-18
;; PRIOR APPLICATION NUMBER: US 60/074,788
;; PRIOR FILING DATE: 1998-02-18
;; PRIOR APPLICATION NUMBER: US 60/094,190
;; PRIOR FILING DATE: 1998-07-27
;; NUMBER OF SEQ ID NOS: 33142
;; SEQ ID NO 10401
;; LENGTH: 588
;; TYPE: DNA
;; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-10401

Alignment Scores:
Pred. No.: 0.113 Length: 588
Score: 114.00 Matches: 54
Percent Similarity: 40.57% Conservative: 32
Best Local Similarity: 25.47% Mismatches: 54
Query Match: 9.11% Indels: 72
DB: 1 Gaps: 9

US-09-252-991A-26292 (1-245) x US-09-252-991A-10401 (1-588)

OY 61 GluSerAlaArgGlyLysLeuLeuGlnThrAlaAlaHisLeuPheArgSerLysGlyTrp 80
DB 52 CAGAGAACCGCGCGCGGTGCTGTCGAGAGCGTCCGCGCGCTTCCGACGAGCGCGTC 111
OY 81 GluArgThrThrValArgAspLeuAlaSerAlaValGlyIleGlnSerGlySerIlePhe 100
DB 112 GCGCGCACCGGCTGACACCGCTGATGAGCGCTGCGCGCTGACCCATGCGCGCTTCAC 171
OY 101 HisHisPheLysSerLysAspGluIleLeuArgSerValMetGluGluThrIleLeuTrp 120
DB 172 GCGCATCTTAAGTCCAGAGACGACCTGTG-----GAAACCGCTTGGCG 216
OY 121 AsnThrAlaLeu-----MetArgAlaAlaLeuAlaAspAlaGluAspLeuArg 136
DB 217 CATGCGCGCGCGCACTGACGAGAAATCACCGCGCGCTGCGGAGCGGAA----- 267
OY 137 GluArgValLeuGlyLeuIleLeuArgGlyGluLeuGlnSerIleMetClyLysThrGly 156
DB 268 -----CGA 270
OY 157 AlaMetAlaValLeuValTrpArgSer----- 167
DB 271 CCGCTGGCGCTGTGATGACGATGCTGTGCGCGCGCTGACCGGATACCGCGCGCC 330
OY 168 -----LeuSerAlaGluGlyGlnAlaTrpIleLeuGlyLeuArg 180
DB 331 GCGTCCGCTGCGCGACCTGTGCGGGAA-----CTGCGCGAGCGCGC 375
OY 181 -----AspIleTrpGluGlnMetTrpLeuAspValLeuGlyGlnAla 194
DB 376 ACGCGAGCGCGACACCGACGATCGTGCACAGCGCGCTGCGCATGATC---CAAGCG 432
OY 195 ArgLeuAlaGlyTrpCysGlnGlyAsp---ProPheIleLeuArgArgPheLeuThrGly 213
DB 433 GCGCTGAGAGCGGAGAGCGACGAGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 492
OY 214 AlaLeuSerTrpThrThrThrTrpPheArgProGluGlyPrometSerLeuAspGlnLeu 233
DB 493 GCGGTGCAACGTGCGCGAGC-----GTG 516
OY 234 AlaGluGluAlaLeuAlaValIleLysAspAla 245
DB 517 CAGATGAGGCGCTGCGCAACGATACTGAGAGCG 552

RESULT 10
US-09-252-991A-9166/C
; Sequence 9166, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:

; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 3541
 ; LENGTH: 1074
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-3541

Alignment Scores:

Pred. No.:	0.0183	Length:	1074
Score:	131.00	Matches:	54
Percent Similarity:	41.94%	Conservative:	24
Best Local Similarity:	29.03%	Mismatches:	60
Query Match:	10.46%	Indels:	48
DB:	1	Gaps:	8

US-09-252-991A-26292 (1-245) x US-09-252-991A-3541 (1-1074)

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Y 63 ALAARGLYLSTLEUENGLNTHRAALAHSLAEPHEARGSERLYSGLYTYRGLUARG 82
    ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 1011 TCCCGGAGAGAGCTTCCAGCGCTCCGCCGACCTTCCGTGCTACGCGCTACACGCG 952
    ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
QY 83 THRTHTVALARGASPLEUALASERIALAVALGYLEGLNSERGLSERILEPHEHSHS 102
    ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 951 ACCACCATGACATGCTGCTCCAGCGCTGCGCTGACCAAGGCGCTGCTACACCAT 892
    ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
QY 103 PHELYSERLYASPLULEULEUARGSERVALMETGLUGLTHR 117
    ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 891 TACCGAACAGAGACCTTGCTCCGCGAGCTTCTGCAAGACCAACGAGCGGCTCGCC 832
    ::::: ::::: ::::: ::::: ::::: ::::: :::::
QY 118 -----LLEUTYRASNTHRALALEU 124
    ::::: ::::: ::::: ::::: ::::: :::::
Db 831 GAGACGCTCTTACGATCGCTACGACCGCGCTGACGCGCGCGAGCGCGCTGAAAAA 772
    ::::: ::::: ::::: ::::: ::::: :::::
QY 125 -----METARGALAHALALEUALASPLAAGLUASPLEUARGLUARGYALLEUGLYLEU 142
    ::::: ::::: ::::: ::::: ::::: :::::
Db 771 CTCGGCCGAGAGCGCGCGCTGTTTCAGAGGACAGCATCGCTGCTGATGAGCGCTG 712
    ::::: ::::: ::::: ::::: ::::: :::::
QY 143 ILE-----ARGCYSLULEU-----GLNSERILEMET 151
    ::::: ::::: ::::: ::::: ::::: :::::
Db 711 GTCCGGCTGAGACCGCCAGCATGTGCTCCAGCAGCATGAGCGCGCGCATCCGACATTTCC 652
    ::::: ::::: ::::: ::::: ::::: :::::
QY 152 GLYGLYTHRGYGLUALAMETALAVALLLEUVALTYRGLUTPRARGSERLEUSERIALAGLU 171
    ::::: ::::: ::::: ::::: ::::: :::::
Db 651 GACGACTGGCGGACAGCTTCGCGCCAGCTC-----TACCGCCGCGGCTTCGACGAG 601
    ::::: ::::: ::::: ::::: :::::
QY 172 GLYGLNALATYRILEULEUYLEUARGASPIIETRYGLUGLIMETTRPLEUASPVALLEU 191
    ::::: ::::: ::::: ::::: :::::
Db 600 GCGCAGGCGCTGAGCGCGGC-----CGGCACACTGGTGGCTGATTTTCGAA 556
    ::::: ::::: ::::: :::::
QY 192 GLYGLUALARGYLEUALA-----GLTYRCYSGLNGLYASPRPROPHE 205
    ::::: ::::: ::::: :::::
Db 555 GCGCGCATCTGCTGCGCGGCGCATGTGCGGAGCGCGCGGCTATATCATGCGC----- 505
    ::::: ::::: ::::: :::::
QY 206 ILELEUARGRPHLEU 211
    ::::: ::::: :::::
Db 504 GTCACCCGCGGAGCGCTG 487
  
```

RESULT 7

; US-09-252-991A-8799
 ; Sequence 8799, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUSINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 10/136.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 8799
 ; LENGTH: 906
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-8799

Alignment Scores:

Pred. No.:	0.14	Length:	906
Score:	117.00	Matches:	54
Percent Similarity:	38.46%	Conservative:	36
Best Local Similarity:	23.08%	Mismatches:	82
Query Match:	9.35%	Indels:	62
DB:	1	Gaps:	9

US-09-252-991A-26292 (1-245) x US-09-252-991A-8799 (1-906)

```

QY 18 ALAALAGLYARGALASPGIUALARGHLSARGALALASPRAPROGLULYSGLYTYR 37
    ::::: ::::: ::::: ::::: ::::: :::::
Db 20 TCGGCTGCGCGGCTCCAGCGGAACCGCGGACGAGGAGAGCAATTCACATACGCT 79
    ::::: ::::: ::::: ::::: :::::
QY 38 ALALEU----- 39
    :::::
Db 80 GCGTATGTCAAAAATCATGAGACATACGACGCTATGTCATATTATCTGAACCCCTTC 139
    :::::
QY 40 -----ASPSPLINLYSLAARGGLUVALMETLEUGLULEUVALAATHRGLYGLN 56
    ::::: ::::: ::::: :::::
Db 140 GCCACCCGGAGACCTGCGATGCGCCAGAGCCTCGCGCGCGAGTGAATC----- 187
    ::::: ::::: ::::: :::::
QY 57 LEUTHRASPRPROGLUBSERIALARGLYLSTLEUENGLNTHRALAHSLAEPHEARG 76
    ::::: ::::: ::::: :::::
Db 188 -----GAGGAACCCGCGGCAAGCTGATGAGCGCGCGCGGCGGAGGTTTCGCC 235
    ::::: ::::: ::::: :::::
QY 77 SERLYGLYTYRGLUARGHTRHVALARGASPLEUALASERIALAVALGYLEGLNSER 96
    ::::: ::::: ::::: :::::
Db 236 GACACGCGCTACCGCGCGCTGATGAGCAAGTACACCGCGCGCTTCACCGCG 295
    ::::: ::::: ::::: :::::
QY 97 GLYSERILEPHEHSHSPHELYSERLYASPLIULEUARGSERVALMETGLUGLU 116
    ::::: ::::: ::::: :::::
Db 296 GCGCGCTGATATACCATCTTCGCGGACAGAAAGGCTGCTGCGCGCGGTGCGACGAG 355
    ::::: ::::: ::::: :::::
QY 117 THRTLEUTYRASNTHRALALEUMETARGALALALEUALASPLAAGLUASPLEU 135
    ::::: ::::: :::::
Db 356 ATCGACGACGAGATGATCTTCGCTGCGCGCATCTGCTGCGCGGAGGACGCTCTGG 415
    ::::: ::::: :::::
QY 136 -----ARGGLUARGYALLEUGLYLEUILEARGCYSGIULEUGLN 148
    ::::: ::::: :::::
Db 416 AGCGGCTTCGCGCTACAAACCGGCGCTACCTGGAATGCGCTGGAAGCGGAATCCAG 475
    ::::: ::::: :::::
QY 149 SERILEMETGLYTHRGYGLUALAMETALAVALLEU-----VAL 162
    ::::: ::::: :::::
Db 476 CGCATGCTC-----CTGCGCGATGCGCGCGCATCTCTGCGGACCGCGAGCGAGCGC 529
    ::::: ::::: :::::
QY 163 TYRGLUTPRARGSERLEUSERIALA---GLUGLYNALATYRILEULEUGLYLEUARGASP 181
    ::::: ::::: :::::
Db 530 AGCCAACTGGCTGCTGCTAAGCTGATGACCGGCGCAA-----CTGCGCGAA 574
    ::::: ::::: :::::
QY 182 ILETYRGLUGLIMETTRPLEUASPVALLEUGLYGLUALARGLEUALAGLYTYRCSGLN 201
    ::::: ::::: :::::
Db 575 CTGATGACAGC-----GGCGCGCTCGC-----CGC 601
    ::::: :::::
QY 202 GLYASPRPROPHLEULEUARGRPHLEUHTHGLYALALEU 215
    ::::: :::::
Db 602 ACCGAGCGGAGCGCGCTGCGCTGCTGCTCAAGCGGCGCGCTG 643
  
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RESULT 8

; US-09-252-991A-8914
 ; Sequence 8914, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

Pred. No.: 0.000958 Length: 732
 Score: 145.00 Matches: 66
 Percent Similarity: 37.65% Conservative: 27
 Best Local Similarity: 26.72% Mismatches: 78
 Query Match: 11.58% Indels: 77
 DB: 1 Gaps: 11

US-09-252-991A-26292 (1-245) x US-09-252-991A-10194 (1-732)

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Oy 2 ProthSerThrCysGlyAlaIleProArgProValGlySerTyrGlyAlaIleArg 21
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 10 CCGAGCGCGCTCTGTGAGGCTTCCACG-----AGCGGCGCT 48
Oy 22 AlaAspLysArgHisArgAlaAlaAspAspProGluSerGlyTyrSerAlaLeuAspAsp 41
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 49 TGC-----CGGCAC-----GCTGCGTGGCGCGCGCATTTGAGAGAGCTCATG----- 93
Oy 42 GluLysAlaArgGluValMetLeuGluLeuValAlaThrGlyGluLeuThrAspProGlu 61
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 94 CGCGGTACCAAGAA-----GACGCGAA 117
Oy 62 SerAlaArgGlyLysLeuLeuGlnThrAlaAlaHisLeuPheArgSerLysGlyTyrGlu 81
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 118 CAGACCGCGCTCAAGATCATCGCGCGCTCGACGCTTTCACCGCACCGCATATTGC 177
Oy 82 ArgThrValArgAspLeuAlaSerAlaValGlyIleGlnSerGlySerIlePheHis 101
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 178 AACACACCGCTGGCGATGATGCGCGAGCGCGCGCTTTCACCGCGCATTTACACG 237
Oy 102 HisPheLysSerLysAspGluIleLeuArgSerValMetGluGluThrIleLeuTyrAsn 121
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 238 CACTTCAAGACAGAGACAG----- 258
Oy 122 ThrAlaLeuMetArgAlaAlaLeuAlaAspAlaGluAspLeuArgGluArgValLeuGly 141
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 259 -----CTGACGAAGCGGCTGCTGCTACTCCAGAGCGCGCTGAGACCTGATTCGAG 312
Oy 142 LeuIleArgCysGluLeuGlnSerIleMetGlyIleThrGlyGluAlaMetAlaValLeu 161
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 313 -----CAGAGTCGCGCAGCTGGCGGTAGCCGCGCGCGCTGGCGTGGACACATTC 360
Oy 162 ValTyrGluTyrArgSerLeuSerAlaGluGlyAlaTyrIleLeuGlyLeuArgAsp 181
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 361 GTCGCGCAATGCTTCCGCTCTGCTGACGAGCGCTGTATTCG-GCAGTCTTCGAGAT 419
Oy 182 IleTyrGluGlnMetTyrPheAsp----- 189
Db 420 CTGCTGACAA-----GACCGAATCATCCGCGCAGATGCGAGCACCTGAAACG 470
Oy 190 -----ValLeuGlyGluAlaArgLeuAlaGlyTyr 199
Db 471 CGAAGCGAGCTCACCGCTGCTGATGTCGATTCGTGAGAGCTGAT----- 518
Oy 200 CysGlnLysAspProPheIleLeuArgArgPheLeuThrGlyAlaLeuSerTyrThr 219
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 519 TGGCCAAAGC-----GCACGCGATGAGAGATCGCGCATCATCAGCTGCTGCT 566
Oy 220 ThrTyrPheArgProGluGly 226
Db 567 GCTCTATTTCAGCCTGATGG 587

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RESULT 5
 US-09-252-991A-3553
 ; Sequence 3553, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252.991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 3553
 ; LENGTH: 651
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-3553

Alignment Scores:
 Pred. No.: 0.008 Length: 651
 Score: 131.00 Matches: 54
 Percent Similarity: 41.94% Conservative: 24
 Best Local Similarity: 29.03% Mismatches: 60
 Query Match: 10.46% Indels: 48
 DB: 1 Gaps: 8

US-09-252-991A-26292 (1-245) x US-09-252-991A-3553 (1-651)

```

Oy 63 AlaArgGlyLysLeuLeuGlnThrAlaAlaHisLeuPheArgSerLysGlyTyrGluArg 82
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 109 TCCCGCAGCGCTTCTTCACGCGCTGCGCGCACCTTCGCTGACGCTACACAGCC 168
Oy 83 ThrThrValArgAspLeuAlaSerAlaValGlyIleGlnSerGlySerIlePheHis 102
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 169 ACCACATGAGCATGCTGTCACGCGCTGCGGCTTGAACCAAGCGCTGTTCTACCAT 228
Oy 103 PheLysSerLysAspGluIleLeuArgSerValMetGluGluThr----- 117
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 229 TACCCGAACAGGAAGCTGCTCCGACGCTTCTCGAATGACCAACACGCGCTGCGC 288
Oy 118 -----IleLeuTyrAsnThrAlaLeu----- 124
Db 289 GAGACGCTTTCACATTCGCTTACGACCGCGCTGTGACCGCGCGCGCGCTGGAANA 348
Oy 125 -----MetArgAlaAlaLeuAlaAspAlaGluAspLeuArgValLeuGlyLeu 142
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 349 CTCGCGCGCAAGCGCGCGCGCTGTTTCACAGACGACAGCATCGGCTGCTGATGGCGTG 408
Oy 143 Ile-----ArgCysGluLeu-----GlnSerIleMet 151
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 409 GTCCGCTCGACGCCAGCTATGTCGACAGCAGCTGATGCGCGCATCCGAGTTCTC 468
Oy 152 GlyGlyThrGlyGluAlaMetAlaValLeuValTyrGluTyrArgSerLeuSerAlaGlu 171
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 469 GACGACTGGCGCAAGCTTGGCCAGCTC-----TACCGCGCGCTTGGACGAG 519
Oy 172 GlyIleAlaTyrIleLeuGlyLeuArgAspIleTyrGluGlnMetTyrPheAspValLeu 191
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 520 GCGCAGGCGCTGAGCGCGG-----GCGCACTGTGGTGGATTTGAA 564
Oy 192 GlyIleAlaArgLeuAla-----GlyTyrCysGlnGlyAspProPhe 205
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 565 GGCCCAATCTGCTGCGCGCATGATGCGAGCGCGGCTATATGATGTC----- 615
Oy 206 IleLeuArgArgPheLeu 211
Db 616 GTCACCGCGGCGCGCTG 633

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RESULT 6
 US-09-252-991A-3541/C
 ; Sequence 3541, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252.991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18

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Db 181 GAAAGCGCCGCGGACCTCTGACAGCCCGCCGACCTGTCGAGCAAGGCGTAC 240
Oy 81 GUATGThrThValArgAspLeuAlaSerAlaValGlyIleGlnSerGlySerIlePhe 100
Db 241 GAACGACACGACGTCGCGGACCTGCGCCGCGCGGTCGATCCAGTCCGGACGATCTTC 300
Oy 101 HishSpheYsSerLysAspGluIleLeuArgSerValMetGluGluThrIleLeuYr 120
Db 301 CATCACTTCAAGAGAGATAGATCTCTGCGTGGTGGATGGAAGAACATCTCTAC 360
Oy 121 AsnThrAlaLeuMetArgAlaAlaLeuAlaAspAlaGluAspLeuArgGluArgValLeu 140
Db 361 AACACCGCCCTGAGCGCGCGCCCTGCGCCGACCGCGAGACCTGCGGACGCGGTGCTG 420
Oy 141 GlyLeuIleArgCysGluLeuGlnSerIleMetGlyGlyThrGlyAlaMetAlaVal 160
Db 421 GGAATGATCCCTCGACGACTCATCTATGAGCGGTACCGCGGAGGCGCATGCGCGGTG 480
Oy 161 LeuValIleGluThrPargSerLeuSerAlaGluGlyAlaIleGlyIleLeuGlyLeuArg 180
Db 481 CTGCTCTACAGAGTGGCGCTGCTCGCGCGAGGCGGAGCGGTACATCTCGCGCTGCGC 540
Oy 181 AspIleTyrGluGlnMetIleLeuAspValLeuGlyGluAlaArgLeuAlaGlyTyrCys 200
Db 541 GACATCTACGACAGATGTGGCTGAGCTGGGGAGGCGCGGTGCGCTGACTGAC 600
Oy 201 GlnGlyAspProPheIleLeuArgArgPheLeuThrGlyAlaLeuSerTyrThr 220
Db 601 CAGGGCGATCCGTCATCTCTGCGCGCTCTCTACCGCGCGGTCTCTGACACACCGCC 660
Oy 221 TrpPheArgProGluGlyProMetSerLeuAspGlnLeuAlaGluGluAlaLeuAlaLeu 240
Db 661 TGGTTCGCTCGGAGAGCGCATGATCTCGATCAGCTGCGCGAGAGAGCGCTGCGCTG 720
Oy 241 ValIleLysAspAla 245
Db 721 GTGATCAAGGAGCGCC 735

RESULT 2
US-09-252-991A-9640
; Sequence 9640, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9640
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9640

Alignment Scores:
Pred. No.: 1.02e-11 Length: 402
Score: 250.00 Matches: 47
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 19.97% Indels: 0
Gaps: 0

US-09-252-991A-26292 (1-245) x US-09-252-991A-9640 (1-402)
Oy 1 MetProThrSerThrCysGlyAlaIleProArgProValGlyIleTyrGlyAlaGly 20

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Db 261 ATGCCGACACACTTGGCGGGGCAATCCGAGCGCGGTGCGCAATAACGAGCGCGCGG 320
Oy 21 ArgAlaAspGluArgHisArgAlaAlaAspAspProGluYsGlyTyrSerAlaLeuAsp 40
Db 321 CCGCGGATGAGCGGACCGGACCGCGCGCATCGGAAAAAGGGGTACTGAGCTTGAC 380
Oy 41 AspGlnLysAlaArgGluVal 47
Db 381 GATCAGAAAGCCCGGAAGTG 401

RESULT 3
US-09-252-991A-9616/c
; Sequence 9616, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9616
; LENGTH: 2064
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9616

Alignment Scores:
Pred. No.: 4.22e-08 Length: 2064
Score: 216.00 Matches: 40
Percent Similarity: 100.00% Conservative: 0
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Query Match: 17.25% Indels: 0
Gaps: 0

US-09-252-991A-26292 (1-245) x US-09-252-991A-9616 (1-2064)
Oy 1 MetProThrSerThrCysGlyAlaIleProArgProValGlyIleTyrGlyAlaGly 20
Db 122 ATGCCGACACACTTGGCGGGGCAATCCGAGCGCGGTGCGCAATAACGAGCGCGCGG 63
Oy 21 ArgAlaAspGluArgHisArgAlaAlaAspAspProGluYsGlyTyrSerAlaLeuAsp 40
Db 62 CGCGGATGAGCGGACCGGACCGCGCATCTCGGAAAAAGGGGTACTGAGCTTGAC 3

RESULT 4
US-09-252-991A-10194
; Sequence 10194, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 10194
; LENGTH: 732
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-10194

Alignment Scores:

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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 30, 2003, 06:59:07 ; Search time 0.001 Seconds

(without alignments)

147,980 Million cell updates/sec

Title: US-09-252-991A-26292

Perfect score: 1252

Sequence: 1 MPTSTGATPRPVGKYGAG.....GPMSLDQLAEALALVIYKDA 245

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Ygapop	10.0	Ygapext	0.5
Fgapop	6.0	Fgapext	7.0
Delop	6.0	Delext	7.0

searched: 1 segs, 302 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1 summaries

Command line parameters:

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-NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -NCPU=6 -NO_XLPXY
-NEG SCORES=0 -LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : us-09-966-608-1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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us-09-966-608-1

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Score:	429.00	Matches:	84
Percent Similarity:	94.00%	Conservative:	10
Best Local Similarity:	84.00%	Mismatches:	6
Query Match:	34.27%	Indels:	0
DB:	1	Gaps:	0

US-09-252-991A-26292 (1-245) x us-09-966-608-1 (1-302)

QY 87 AspleualaSerAlaValAlGlyIleGlnSerGlySerIlePheHisHisPheLysSerLys 106
DB 2 GATCTGGCCACGCCGCGATCCAGTCACGCGGACGACATCTTCACTTCAAGACGAG 61

QY 107 AspgIleLeuArgSerValMetGluIuThrIleLeuTYraSnThrAlaLeuMetArg 126
DB 62 GATGAGATATTGCGTGGCGGATGAGGAAACCATCCATTACACACCGCATGATGCGC 121
QY 127 AlaAlaLeuAlaAspAlaGluAspLeuArgGluArgValLeuGlyLeuIleArgCysGlu 146
DB 122 GCTTCACCTGGAGGAGGCGCAGCAGCAGCGCCGCGTGGCTGGCGCTGATCCGCTGGCAG 181
QY 147 LeuGlnSerIleMetGlyGlyThrGlyGluAlaMetAlaValLeuValTYrGluTrpArg 166
DB 182 TTGCAGTCGATCATGCGCGCAGTGGCGGAGCCATGCGCGTGTCTACGAAATGCGCGC 241
QY 167 SerLeuSerAlaGluGlyGlnAlaIleTYrIleLeuGlyLeuArgAspIleTYrGluGlnMet 186
DB 242 TCGCTGTGGCCGAAAGCGCAGCGCATCGTGGCGCTGCGTGAAGTGTATGACGACAGATC 301

Search completed: April 30, 2003, 06:59:07
Job time : 0.001 secs

